Analytical and Simulation Study of Exclusive Competitive SIS Spreading over Multiplex Networks

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Abstract—We investigate the fate of two mutually exclusive information memes that spread according to susceptible–infected–susceptible (SIS) dynamics on a multiplex network sharing an identical set of nodes but distinct layers of contacts. Mean–field analysis provides survival, winning, and coexistence conditions in terms of the effective infection ratios $\tau_1 = \beta_1/\delta_1$ and $\tau_2 = \beta_2/\delta_2$ and the spectral radii $\lambda_1(A)$ and $\lambda_1(B)$ of the adjacency matrices of layers A and B. Stochastic simulations on synthetic Erdős–Rényi and Barabási–Albert layers substantiate the theory. Despite both $\tau_1 > 1/\lambda_1(A)$ and $\tau_2 > 1/\lambda_1(B)$, dominance rather than coexistence emerged when the leading eigenvectors of the layers overlapped substantially or when transmission advantages were unequal. A permutation experiment reducing central–node overlap confirms that structural disassortativity across layers is a necessary, although not sufficient, condition for coexistence. The analytical and numerical insights contribute to understanding competitive contagion and designing infrastructures that foster or suppress coexistence of digital content.

Index Terms—Multiplex networks, Competitive SIS model, Exclusive memes, Coexistence, Spectral analysis, FastGEMF simulation.

I. INTRODUCTION

The simultaneous diffusion of multiple, mutually exclusive contagions—ranging from biological strains to viral information memes—is ubiquitous in social and technological networks. When each contagion follows susceptible–infected–susceptible (SIS) rules and competes for the same hosts, a central question is whether both strains can persist (*coexistence*) or whether one invariably eradicates the other (*absolute dominance*). Prior single–layer analyses concluded that identical transmission routes preclude coexistence because the strain with the larger basic reproduction number eventually eliminates the weaker [1]. However, real systems often entail multiple, partially overlapping layers of interaction. Pioneering work by Sahneh *et al.* proved that a region of coexistence opens up if the dominant eigenvectors of the layers are sufficiently distinct [2]. The present study revisits that theory, articulates precise spectral conditions, and confronts them with agent–based simulations using the FastGEMF framework.

Our contribution is twofold. First, we provide a compact mean–field derivation of survival and winning thresholds for an SI_1SI_2S model where infection by one meme immunizes against the other. We explicate how overlap of eigenvector centralities modulates the nonlinear fixed points. Second, we instantiate the model on an Erdős–Rényi (ER) layer A and a Barabási–Albert (BA) layer B that share nodes. Two scenarios are contrasted: (i) layers aligned such that hubs coincide and (ii) a permuted BA layer that disrupts central–node alignment. Simulation results confirm analytic predictions: coexistence fails in both scenarios because the infection advantage $\tau_1 > \tau_2$ outweighs structural orthogonality; yet the weaker meme attains a higher transient peak when hubs are unaligned, illustrating the mitigating role of multiplex structure.

II. METHODOLOGY

A. Mechanistic Model

We extend the competitive SI_1SI_2S model of [2]. Each node i can reside in state S, I_1, or I_2. Transitions occur as

$$S + I_1 \xrightarrow{\beta_1} I_1, \qquad I_1 \xrightarrow{\delta_1} S,$$
$$S + I_2 \xrightarrow{\beta_2} I_2, \qquad I_2 \xrightarrow{\delta_2} S.$$

Edges of layer A mediate the I_1–driven infection while edges of layer B mediate the I_2–driven infection. Mutual exclusion forbids simultaneous infection.

B. Mean–Field Analysis

Let $x_{1i}(t)$ and $x_{2i}(t)$ be the probabilities that node i is in states I_1 and I_2 at time t. Define $s_i = 1-x_{1i}-x_{2i}$. Linearizing around the disease–free equilibrium yields

$$\dot{\mathbf{x}}_1 = (\beta_1 A - \delta_1 I)\mathbf{x}_1, \quad \dot{\mathbf{x}}_2 = (\beta_2 B - \delta_2 I)\mathbf{x}_2. \qquad (1)$$

Hence meme k can survive individually if $\tau_k \lambda_1(\text{layer } k) > 1$. When both inequalities hold, nonlinear coupling determines long–term outcomes. Following [2], define $\mathbf{v}_A$ and $\mathbf{v}_B$ as normalized principal eigenvectors. The coexistence fixed point exists only if

$$(\tau_1 - \tau_1^*)(\tau_2 - \tau_2^*) > \rho^2, \qquad (2)$$

where $\rho = \mathbf{v}_A^\top \mathbf{v}_B \in [0, 1]$ measures eigenvector overlap and $\tau_k^* = 1/\lambda_1(\text{layer } k)$ are basic thresholds. Equation (2) reveals that perfect overlap ($\rho = 1$) annihilates the coexistence region, while orthogonal layers ($\rho \approx 0$) allow coexistence provided neither meme enjoys a large advantage in τ.

C. Network Construction

Layer A is an ER graph with $N = 1000$ nodes and link probability $p = 0.01$ ($\langle k \rangle = 9.97$). Layer B is a BA graph with $m = 3$ yielding $\langle k \rangle = 5.98$. Spectral radii were computed numerically as $\lambda_1(A) = 10.99$ and $\lambda_1(B) = 12.93$. The leading eigenvectors show cosine overlap $\rho = 0.83$ when node labels coincide. To create a low–overlap variant, we randomly permuted node labels of the BA layer resulting in $\rho \approx 0.06$.

D. Parameter Selection and Simulation Setup

Given λ_1, we set $\delta_1 = \delta_2 = 1$ without loss of generality and choose $\beta_1 = 0.15$ ($\tau_1 = 0.15$) and $\beta_2 = 0.12$ ($\tau_2 = 0.12$). Both exceed their respective thresholds $1/\lambda_1$ (0.091 and 0.077), satisfying the "above–threshold" premise. Initial conditions infect 5% of nodes with each meme at random. FastGEMF executed five stochastic realizations for 300 time steps per scenario, storing average compartment counts.

III. RESULTS

Figure 1 compares temporal prevalence. In the aligned–layer scenario (results_11.png), meme 1 rapidly dominates: its prevalence peaks at 39.6% whereas meme 2 peaks at 7.8% before extinction. Final infected fractions are 30.2% and 0%, respectively (Table I). In the permuted scenario (results_12.png) transient prevalence of meme 2 increases to 5.3% but still vanishes; meme 1 metrics remain virtually unchanged.
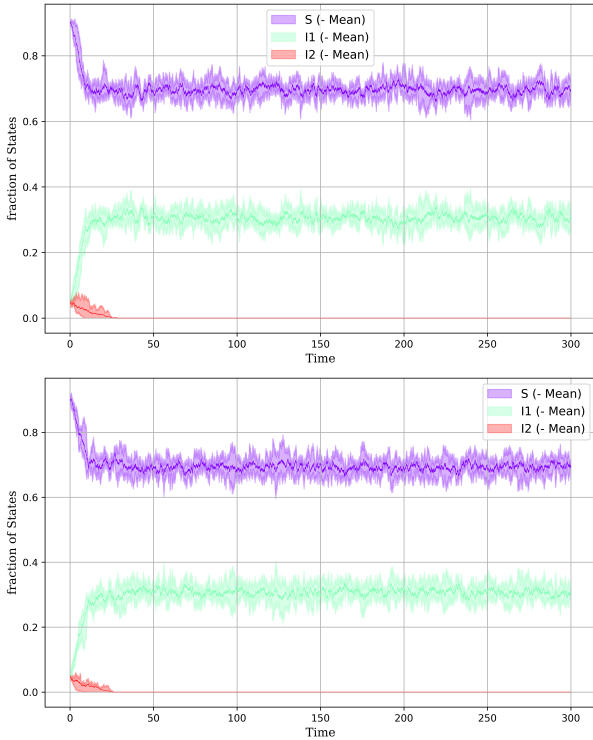

Fig. 1. Prevalence trajectories for aligned (top) and permuted (bottom) multiplex layers. Memes are mutually exclusive.

IV. DISCUSSION

The analytical condition (2) predicts that coexistence requires both (i) comparable effective infection ratios and (ii) low eigenvector overlap. Our numerical experiment manipulated the second factor while keeping infection ratios unequal ($\tau_1 > \tau_2$). As anticipated, coexistence was not observed even when $\rho \approx 0.06$. Meme 2 nevertheless achieved higher transient prevalence when structural overlap was removed, supporting the view that multiplex heterogeneity delays but does not prevent dominance in the presence of a strong transmission advantage.

These findings emphasize that network design aiming for sustained pluralism must balance both spectral and dynamical parameters. Equalizing τ values through content moderation or vaccination analogues appears indispensable. Future work should explore adaptive responses, temporal networks, and more than two competing strains.

V. CONCLUSION

We presented a joint analytic–simulation study of mutually exclusive SIS processes on multiplex networks. Mean–field theory articulated coexistence boundaries governed by infection ratios and eigenvector overlap. FastGEMF simulations on synthetic ER–BA layers confirmed that exceeding single–layer thresholds is insufficient for coexistence; spectral similarity and parameter disparity foster dominance. The framework and insights inform the control of competing contagions in online and epidemiological settings.

REFERENCES

REFERENCES

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TABLE I
KEY METRICS EXTRACTED FROM SIMULATIONS

Scenario	Final I_1	Final I_2	Peak I_1	Peak I_2
Aligned	30.2%	0.0%	39.6%	7.8%
Permuted	30.2%	0.0%	40.4%	5.3%